

Package ‘sdStaf’

October 14, 2022

Type Package

Title Species Distribution and Stability Future Models

Version 1.0.2

Date 2018-10-29

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Description Functions for post processing the outcomes of ecological niche models. It further include methods to build stability maps based on species distribution models under climate change projections and to reduce environmental data.

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Encoding UTF-8

LazyData true

RoxygenNote 6.1.0

Depends methods, stats, dplyr, ggplot2, R (>= 2.10)

Imports sp, rgdal, rgeos, rasterVis, tidyr, raster, dismo

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

Date/Publication 2018-10-30 10:40:02 UTC

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`cor.show` *Correlogram plot*

Description

Returns plot with correlation values among predicted variables.

Usage

```
cor.show(r, rm = FALSE, var.rm)
```

Arguments

<code>r</code>	EnvimRed-class.
<code>rm</code>	logical. If TRUE, allows remove some variables from input data set. (default = FALSE)
<code>var.rm</code>	variables names of input data set. Using <code>colnames(RasterStick)</code> , Where <code>RasterStick</code> is <code>RasterStack*</code> object.

Details

Correlation matrix based on pearson.

Value

Correlogram plot

See Also

[reduce.env](#)

EnvimRed-class *myRefClass*

Description

`myRefClass`

Slots

`cropla` A RasterBrinck
`m.env` A Matrix
`project` A List

phytotoma

Peruvian Plantcutter Occurrence Data

Description

A dataset containing occurrence record locations of Peruvian plantcutter (*Phytoma raimondii*), endemic species of Dry forest in northern Peru. These records have been examined to check for accurate species identification.

Usage

```
data(phytotoma)
```

Format

A data frame with 50 rows and 3 columns

Details

- sp.name species name
- x Longitude
- y Latitude

reduce.env

Reduce environmental data

Description

This function allows reduce environmental data clipping by mask or buffer area

Usage

```
reduce.env(env, transfer = NULL, occ_data, mask)
```

Arguments

env	RasterStack* objet.
transfer	List of rasterstack object
occ_data	A data.frame of occurrence records. It must include two column based on latitude and longitude.
mask	Cropped mask, must be shapefile (.shp), readOGR.

Details

Reduce the correlation among predicted variables either buffer zone, or clipping mask.

Provide reduce objet with cut predicted variables and data.frame for the values of each point of occurrence of them.

Value

@crop RasterStack* Objet

@m.env data.frame of environmental values to occurrence localities.

See Also

[cor.show](#)

Examples

```
# Phytotoma occurrence data
data(phytotoma)

# Complement
library(dismo)
predictor <- stack(list.files(path=paste(system.file(package="dismo"),'/ex', sep=''),
  pattern='grd', full.names=TRUE ))

maskM <- stim.M(phytotoma[,2:3], 131)

reduce_cut <- reduce.env(env = predictor, occ_data = phytotoma[,2:3], mask=maskM)

# Plot reduce_cut
plot(reduce_cut@cropla$bio1)

# Add points
points(phytotoma[,2:3], pch=16,col='blue')

# Correlogram
cor.show(reduce_cut)
rd <- c('bio1','bio12','bio16','biome','bio8')

# Removing rd-variables on correlogram
cor.show(reduce_cut, rm=TRUE, var.rm = rd)

# Remove rd-variables
var_reduce <- dropLayer(reduce_cut@cropla, rd)

# summary
var_reduce
```

StabEcodist-class	<i>StabEcodist</i>
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Description

StabEcodist

Slots

df A RasterBrinck
map A Matrix

stability	<i>Stability of ecological niche models</i>
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Description

Returns stability niche based on species distribution models and their projections.

Usage

```
stability(current = NULL, project = NULL, thr.value,
          continue = FALSE)
```

Arguments

current	Raster* objet of present distribution. Raster has continue values.
project	RasterStack* object of project distributions. Must have three models with continue values.
thr.value	Cut value (0 — 1) of threshold in order to species distribution.
continue	defines if the species distribution are either binary or continue maps. Default = FALSE.

Value

An object of class 'StabEcodist'

Based on binary maps

Return table with these features: Models and nPixel (frequency of pixel with that feature).

Stability maps based on binary species distirbution, give:

Values of 0 Shows absence

Values of 100 Mentions the lost area

Values [1:100] Shows colonizable area. Different models are defined as numbers (e.g. Value of 1 indicates one models predict gain; Value of 2 indicates two models predict agains)

Values > 100 Shows stability or permanence. Different models are defined as numbers (e.g. value of 101 mentions one model predict stability, value of 102 mentions two models predict stability)

Based on continue maps

Species distribution show different values of stability along of their distributions.

Values of -2 Shows absence

Values [-1 : 0] Shows colonized grade or gain.

Values [0 : 1] Shows stability or permanence

Values of 2 Shows lost area

References

Peterson et al., (2017) Influences of climate change on the potential distribution of *Lutzomyia longipalpis* sensu lato (Psychodidae: Phlebotominae). *International Journal for Parasitology*. 47(10–11):667–74.

<code>stim.M</code>	<i>Build buffer zone to M</i>
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Description

Returns buffer zone based on occurrence data

Usage

```
stim.M(occs, radio, bgeo = NULL, ...)
```

Arguments

<code>occs</code>	data.frame of occurrence data (longitude/latitude).
<code>radio</code>	radio of buffer.
<code>bgeo</code>	Biogeographical layer. Categorical values.
<code>...</code>	Optional features of buffer

Details

To define calibration area is crucial step (Barve et al., 2011), even more with incomplete sample data sometime is complicated, because to get complete sample within geography space is difficult, in these cases is appropriate define M with buffer zone (Peterson et al., 2017); and in other cases it helps to cut the ends of the calibration area based on the maximum dispersion capacity (Atauchi et al., 2018).

Value

SpatialPolygons* object

References

Atauchi et al. (2018). Species distribution models for Peruvian Plantcutter improve with consideration of biotic interactions. *J. avian biology* 2018: e01617. <doi:http://10.1111/jav.01617.>

Barve et al. (2011) The crucial role of the accessible area in ecological niche modeling and species distribution modeling. *Ecol. Mod.* 222:1810–1819.

Peterson et al.(2017) Influences of climate change on the potential distribution of *Lutzomyia longipalpis* sensu lato (Psychodidae: Phlebotominae). *International journal for parasitology.* 45(10-11): 667–674.

Examples

```
# Phytotoma occurrence data
data(phytotoma)

# Build buffer zone
buf_M <- stim.M(occs=phytotoma[,2:3], 100)

# Add points
points(phytotoma[,2:3])
```

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